

# WEST

## Freeform Search

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JPO Abstracts Database  
EPO Abstracts Database  
Derwent World Patents Index  
IBM Technical Disclosure Bulletins

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### Search History

DB Name	Query	Hit Count	Set Name
USPT,JPAB,EPAB,DWPI	119 not 116	22	L21 ←
USPT,JPAB,EPAB,DWPI	119 not 113	24	L20
USPT,JPAB,EPAB,DWPI	118 and 11 and 14	24	L19
USPT,JPAB,EPAB,DWPI (18 or 19) same ((virulence adj factor\$1) or toxin\$1)	11 and 14	377	L18
USPT,JPAB,EPAB,DWPI	115 not 113	919	L17
USPT,JPAB,EPAB,DWPI	14 and (16 same 19)	20	L16 ←
USPT,JPAB,EPAB,DWPI	14 same 16 same 19	21	L15
USPT,JPAB,EPAB,DWPI	112 and database\$1	0	L14
USPT,JPAB,EPAB,DWPI	111 and automata\$3	50	L13 ←
USPT,JPAB,EPAB,DWPI	15 and (16 or 17 or 110)	313	L12
USPT,JPAB,EPAB,DWPI	multiple	765	L11
USPT,JPAB,EPAB,DWPI	DNA with (ampli\$4 or amplification)	79121	L10
USPT,JPAB,EPAB,DWPI	per or "polymerase chain reaction"	15411	L9
USPT,JPAB,EPAB,DWPI	target with (species or microorganisms)	23349	L8
USPT,JPAB,EPAB,DWPI	array or microarray	4342	L7
USPT,JPAB,EPAB,DWPI	14 same (pathogen\$1 or bacteri\$2)	422769	L6
USPT,JPAB,EPAB,DWPI	food or foodborne	12231	L5
USPT,JPAB,EPAB,DWPI	(BENSON-ANDREW-K);	319342	L4
DWPI,EPAB,JPAB,USPT	(BENSON-ANDREW);	0	L3 ←
USPT,JPAB,EPAB,DWPI	((435/6);CCL5.)	0	L2 ←
		8461	L1

09/1639690

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DB Name	Query	Hit Count	Set Name
EPAB.DWPI	113 and (plurality or simultaneous)	3	L14
EPAB.DWPI	13 and 16 and (nucleic acid\$1)	97	L13
EPAB.DWPI	(111 or 19 or 17) and @py<2000	18	L12
EPAB.DWPI	11 and 110 and 15	9	L11
EPAB.DWPI	microorganisms\$1 or "micro-organisms"	42757	L10
EPAB.DWPI	11 and 12 and 18	1	L9
EPAB.DWPI	multiplex	35347	L8
EPAB.DWPI	11 and 12 and 15	20	L7
EPAB.DWPI	probe\$1	81825	L6
EPAB.DWPI	array\$1 or microarray\$1	141177	L5
EPAB.DWPI	array or microarray	141173	L4
EPAB.DWPI	11 and 12	6214	L3
EPAB.DWPI	bacteri\$2 or virus\$2 or pathogen\$1	99990	L2
EPAB.DWPI	food or foodborne	165414	L1

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### Search History

Today's Date: 12/8/2000

DB Name	Query	Hit Count	Set Name
USPT,JPAB,EPAB,DWPI	125 and 18 and 16 and (12 or array)	3	L26
USPT,JPAB,EPAB,DWPI	(6027890 or 5824473 or 6027889 or 6001564 or 5753467 or 5795717).pn.	13	L25
USPT,JPAB,EPAB,DWPI	123 same 16	1	L24
USPT,JPAB,EPAB,DWPI	18 same simultaneous same detect\$3	87	L23
USPT,JPAB,EPAB,DWPI	18 same probe same array	32	L22
USPT,JPAB,EPAB,DWPI	18 same 12	1	L21
USPT,JPAB,EPAB,DWPI	18 same 12 same species	0	L20
USPT,JPAB,EPAB,DWPI	114 same 12	2	L19
USPT,JPAB,EPAB,DWPI	12 same 13 same 18	0	L18
USPT,JPAB,EPAB,DWPI	116 not same (synthesis or sequenc\$3)	6	L17
USPT,JPAB,EPAB,DWPI	16 same 18 same (DNA with puri\$7)	18	L16
USPT,JPAB,EPAB,DWPI	16 and 18 and (DNA with puri\$5)	3834	L15
USPT,JPAB,EPAB,DWPI	simultaneous same species	1382	L14
USPT,JPAB,EPAB,DWPI	14 and 12	0	L13
USPT,JPAB,EPAB,DWPI	14 2 same 12	1631	L12
USPT,JPAB,EPAB,DWPI	14 same2 12	1631	L11
USPT,JPAB,EPAB,DWPI	14 same 12	0	L10
USPT,JPAB,EPAB,DWPI	17 and 18	3	L9
USPT,JPAB,EPAB,DWPI	bacteria	143417	L8
USPT,JPAB,EPAB,DWPI	16 same 13	14	L7
USPT,JPAB,EPAB,DWPI	automa\$3	1049588	L6
USPT,JPAB,EPAB,DWPI	13 and 14	0	L5
USPT,JPAB,EPAB,DWPI	coli same salmonella same listeria	446	L4
USPT,JPAB,EPAB,DWPI	detect\$3 same 12	513	L3
USPT,JPAB,EPAB,DWPI	microarray or "probe array"	1185	L2
USPT,JPAB,EPAB,DWPI	"plurality of species"	0	L1

## WEST

## Freeform Search

Database: **US Patents Full Text Database**  
 JPO Abstracts Database  
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 IBM Technical Disclosure Bulletin

Term: **119 and enrich\$4**

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## Search History

Today's Date: 12/8/2000

DB Name	Query	Hit Count	Set Name
USPT	119 and enrich\$4	15	L21
USPT	118 same bacteria	2	L20
USPT	118 and bacter\$2	66	L19
USPT	116 not thuringiensis	92	L18
USPT	113 not thuringiensis	207	L17
USPT	113 not same sequence\$4	93	L16
USPT	113 same enrich\$4	3	L15
USPT	113 same grow\$3	11	L14
USPT	11 same 13 same (purify or purification)	217	L13
USPT	11 same (pathogen\$1 or bacter\$2) same enrichment	8	L12
USPT	110 same 13	24	L11
USPT	11 same (pathogen\$1 or bacter\$2) same cultur\$3	275	L10
USPT	15 and (pathogen\$1 or bacter\$2)	30	L9
USPT	15 same species	4	L8
USPT	15 same (pathogen\$1 or bacter\$2)	0	L7
USPT	15 same food	0	L6
USPT	14 same detect\$3	43	L5
USPT	11 same 12 same 13	63	L4
USPT	nucleic acid\$1	31403	L3
USPT	microarray\$1 or array\$1	234593	L2
USPT	automat\$3	379589	L1

STN search 09/639690 Dec. 08, 2000  
databases searched, search terms, and selected abstracts

=> d his  
(FILE 'HOME' ENTERED AT 11:39:12 ON 08 DEC 2000)

FILE 'MEDLINE, BIOSIS, AGRICOLA, CAPLUS' ENTERED AT 11:39:23 ON 08  
DEC

2000.  
L1 916 S BENSON A?/AU  
L2 813456 S FOOD OR FOODBORNE  
L3 2555059 S PATHOGEN? OR MICRO-ORGANISM? OR MICROORGANISM?  
OR BACTERI?  
L4 115825 S ARRAY? OR MICROARRAY?  
L5 462876 S PROBE?  
L6 237483 S AUTOMAT?  
L7 77892 S DATABASE?  
L8 269012 S VIRULENCE(W)/FACTOR? OR TOXIN? OR VIRULENCE(W)/GENE?  
L9 26223 S PLURALITY OR MULTIPLEX  
L10 2 S L1 AND L2 AND L3  
L11 318 S L2 AND L3 AND (L4 OR L9)  
L12 0 S L11 AND L6 AND L7  
L13 12 S L11 AND L6  
L14 2 S L11 AND L7  
L15 14 S L13 OR L14  
L16 24 S L11 AND L5  
L17 1358 S TARGET(W)/SPECIES  
L18 24 S L11 AND L16  
L19 0 S L11 AND L17  
L20 170 S L11 AND DETECT?  
L21 47 S L20 AND L8  
L22 1 S L21 AND COLI AND SALMONELLA  
L23 69 S L4 AND L8 AND L2  
L24 37 L10 OR L15 OR L16  
L25 29 DUP REM L24 (8 DUPLICATES REMOVED)

*more terms after page 15*

=> d ibib ab 125 1-

YOU HAVE REQUESTED DATA FROM 29 ANSWERS - CONTINUE? Y/(N)/Y

L25 ANSWER 1 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 2000:742344 CAPLUS  
DOCUMENT NUMBER: 133:318245  
TITLE: Amplification and separation of nucleic acid sequences  
using strand displacement amplification and

bioelectronic microchip technology  
Inventor(s): Nerenberg, Michael I.; Edman, Carl F.; Spargo,  
Catherine A.; Walker, George T.  
Patent Assignee(s): Nanogen/Bection Dickinson Partnership, USA  
Source: PCT Int. Appl., 137 pp.  
CODEN: PIXXD2  
Document Type: Patent  
Language: English  
Family Acc. Num. Count: 1  
Patent Information:

Patent No. Kind Date Application No. Date  
WO 2000062036 A1 20001019 WO 2000-US9711 20000411  
W: CA, JP, US  
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,  
PT, SE  
US 1999-290632 19990412

PRIORITY APPLN. INFO.:  
AB Described and disclosed are devices, methods, and comps. of matter for  
the multiplex amplification and anal. of nucleic acid sequences  
in a sample using novel strand displacement amplification technologies in  
combination with bioelectronic microchip technol. Specifically, a nucleic  
acid in a sample is amplified to form amplicons, the amplicons are  
addressed to specified electronically addressable capture sites of the  
bioelectronic microchip, the addressed amplicons are captured and labeled,  
and then the capture sites are analyzed for the presence of label.  
Samples may be amplified using strand displacement methodologies well known  
invention is also amenable to other amplification methodologies well known  
by those skilled in the art. The capture and label steps may be by a  
method of universal capture with sequence-specific reporter. The label  
method of sequence-specific capture with universal reporter. The label  
may be detected by fluorescence, chemiluminescence,  
electrochemiluminescence, or any other technique well known by those  
skilled in the art. This invention further allows for analyzing multiple  
nucleic acid targets on a single diagnostic platform wherein the nucleic  
acids may be amplified while either in direct contact with microchip  
components or in soln. above the microchip array. Thus, the  
described device and method was used to identify different  
bacteria on the basis of their 16S rRNA. Addnl., multiple patient  
samples were simultaneously analyzed for the presence of the Factor V  
Leiden (R506Q) gene mutation using allele-specific strand-displacement  
amplification (SDA) or anchored SDA. A no. of probes were  
prepd. for exonuclease-ligase strand displacement amplification and  
detection of numerous bacterial genes, e.g., gene eaeA of E.  
coli O157:H7.

REFERENCE COUNT: 4

REFERENCE(S): (1) Adams: US 5641658 A 1997  
(2) Edman: Nucleic Acids Research 1997, V25(24), P4907

CAPLUS  
(3) Heller: US 5605662 A 1997  
(4) Rijks Universiteit Leiden: WO 9521938 A1 1995  
CAPLUS

DUPLICATE 1

L25 ANSWER 7 OF 29 MEDLINE MEDLINE

ACCESSION NUMBER: 2000163995

DOCUMENT NUMBER: 20163995

TITLE: Multiplex PCR for detection and identification of

Lactococcal bacteriophages.

AUTHOR: Labrie S, Moineau S

CORPORATE SOURCE: Department of Biochemistry and Microbiology, Faculte des

Sciences et de Genie, et Groupe de Recherche en Ecologie  
Buccale, Faculte de Medecine Dentaire, Universite Laval,  
Quebec, Canada G1K 7P4.

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (2000 Mar) 66

SOURCE: (3)

987-94.

Journal code: 6K6. ISSN: 0099-2240.

PUB. COUNTRY: United States

Journal: Article: (JOURNAL ARTICLE)

English

LANGUAGE: Priority Journals

FILE SEGMENT: GENBANK-AF152410; GENBANK-AF152411; GENBANK-

OTHER SOURCE: GENBANK-AF152410; GENBANK-AF152411; GENBANK-

AF152412; GENBANK-AF152407; GENBANK-AF152409; GENBANK-AF142414;

ENTRY MONTH: 200006

ENTRY WEEK: 20000605

AB Three genetically distinct groups of Lactococcus lactis phages are

encountered in dairy plants worldwide, namely, the 936, c2, and P335

species. The multiplex PCR method was adapted to detect, in a

single reaction, the presence of these species in whey samples or in phage

lysates. Three sets of primers, one for each species, were designed based

on conserved regions of their genomes. The c2-specific primers were

constructed using the major capsid protein gene (mcp) as the target. The

mcp sequences for three phages (eb1, Q36, and Q44) were determined and

compared with the two available in the databases, those for

phages c2 and bl167. An 86.4% identity was found over the five mcp genes.

The gene of the only major structural protein (msp) was selected as a

target for the detection of 936-related phages. The msp sequences for

three phages (p2, Q7, and Q11) were also established and matched with the

available data on phages sk1, bl170, and F4-1. The comparison of the six  
msp genes revealed an 82.2% identity. A high genomic diversity was  
observed among structural proteins of the P335-like phages suggesting that  
the classification of lactococcal phages within this species should be  
revised. Nevertheless, we have identified a common genomic region in 10  
P335-like phages isolated from six countries. This region corresponded to  
orf17-orf18 of phage r11 and orf20-orf21 of Tuc2009 and was sequenced for  
three additional P335 phages (Q30, P270, and u40). An identity of 93.4%  
within a 739-bp region of the five phages was found. The detection limit  
of the multiplex PCR method in whey was 10(4) to 10(7) PFU/ml  
and was 10(3) to 10(5) PFU/ml with an additional phage concentration step.  
The method can also be used to detect phage DNA in whey powders and may  
also detect prophage or defective phage in the bacterial genome.

L25 ANSWER 8 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 2000.410198 BIOSIS

DOCUMENT NUMBER: PREV200000410198

TITLE: The use of multiplex PCR reactions to

characterize populations of lactic acid bacteria

AUTHOR(S): Yost, C. K. (1), Nattress, F. M.

CORPORATE SOURCE: (1) Lacombe Research Centre, Agriculture and Agri-Food

Canada, 6000 C and E Trail, Lacombe, Alberta, T4L 1W1

SOURCE: No. 2, pp. 129-133. print.

ISSN: 0266-8254.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A rapid, systematic and reliable approach for identifying lactic acid

bacteria associated with meat was developed, allowing for

detection of Carnobacterium spp., Lactobacillus curvatus, Lact. sakei and

Leuconostoc spp. Polymerase chain reaction primers specific for

Carnobacterium and Leuconostoc were created from 16S rRNA oligonucleotide

probes and used in combination with species-specific primers for

the 16S/23S rRNA spacer region of Lact. curvatus and Lact. sakei in

multiplex PCR reactions. The method was used successfully to

characterize lactic acid bacteria isolated from a

vacuum-packaged pork loin stored at 2 degreeC. Seventy isolates were

selected for identification and 52 were determined to be Lact. sakei,

while the remaining 18 isolates were identified as Leuconostoc spp.

L25 ANSWER 12 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1999:530386 BIOSIS  
DOCUMENT NUMBER: PREV199900530386  
TITLE: A multiplex reverse transcription polymerase chain reaction method for the detection of foodborne viruses.

AUTHOR(S): Rosenfield, Soraya I.; Jaykus, Lee-Ann (1)  
CORPORATE SOURCE: (1) Department of Food Science, North Carolina State University, Raleigh, NC, 27695-7624 USA

SOURCE: Journal of Food Protection, (Oct., 1999) Vol. 62, No. 10, pp. 1210-1214.  
ISSN: 0362-028X.

DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB A multiplex reverse transcription polymerase chain reaction (RT-PCR) method was developed for the simultaneous detection of the human enteroviruses, hepatitis A virus (HAV) and Norwalk virus (NV). Poliovirus type 1 (PV1) was chosen as a model for the human enterovirus group. Three different sets of primers were used to produce three size-specific amplicons of 435 bp, 270 bp, and 192 bp for PV1, NV, and HAV, respectively. RT-PCR products were separated by agarose gel electrophoresis, and amplicon identity was confirmed by Southern transfer followed by DNA hybridization using nonradioactive, digoxigenin-labeled internal probes. When tested on mixed, purified virus suspensions, the multiplex method achieved detection limits of 10<sup>2</sup> infectious unit (PV1 and HAV) or RT-PCR-amplifiable unit (NV) for all viruses. With further streamlining efforts such as single tube amplification and liquid hybridization, multiplex PCR offers advantages over cell culture methodology and monoplex PCR because it allows for rapid and cost-effective detection of several human enteric viruses in a single reaction tube.

L25 ANSWER 13 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1999:497873 CAPLUS  
DOCUMENT NUMBER: 132:19267  
TITLE: Semi-automated fluorogenic PCR assays (TaqMan) for rapid detection of Escherichia coli O157:H7 and other Shiga toxinogenic E. coli

AUTHOR(S): Sharma, V. K.; Dean-Nystrom, E. A.; Casey, T. A.  
CORPORATE SOURCE: Enteric Diseases and Food Safety Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, Ames, IA, 50010, USA

SOURCE: Mol. Cell. Probes (1999), 13(4), 291-302  
CODEN: MCPRE6; ISSN: 0890-8508  
PUBLISHER: Academic Press  
DOCUMENT TYPE: Journal

LANGUAGE: English

AB Semi-automated detection of Enterohaemorrhagic Escherichia coli (EHEC) O157:H7 and non-O157:H7 Shiga toxin-producing E. coli (STEC) was achieved using fluorogenic polymerase chain reaction (PCR). These PCR assays were designed to amplify 80, 120 and 150 bp regions of virulence genes stx1, stx2 and eaeA, resp., using specific primers. The fluorogenic probes were used for specific detection of amplified products of stx1 and stx2 genes of STEC, and the eaeA gene of EHEC O157:H7. For multiplex PCR assay, the three sets of primers and fluorogenic probes were included in one reaction to simultaneously amplify and detect any of the three targeted virulence genes. In non-multiplex PCR assay, each of the three virulence genes was amplified and detected in independent reactions. The specificity of these assays was evaluated using suspensions of STEC and other bacterial species lacking stx1, stx2 and eaeA. The multiplex assay detected all STEC harboring any combination of three virulence genes. Three non-multiplex PCR reactions identified types of Shiga toxin genes carried by a STEC and identified STEC as either EHEC O157:H7 or non-O157:H7 STEC. Sensitivity limits of these assays in beef and feces inoculated with EHEC O157:H7 were 5.8 to 580 cfu and 1.2 to 1200 cfu, resp. These assays can be completed within 8-10 h when performed simultaneously or within 13 h if the multiplex assay is used as an initial screen for detecting STEC and the non-multiplex assay is used for subsequent detection of stx1 and stx2 of STEC and eaeA of EHEC O157:H7. (c) 1999 Academic Press.

REFERENCE COUNT: 49  
REFERENCE(S): (2) Bassler, H. Applied and Environmental Microbiology 1995, V61, P3724 CAPLUS  
(3) Beebakhee, G. FEMS Microbiology Letters 1992, V91, P63 CAPLUS  
(4) Bilge, S. Infection and Immunity 1996, V64, P4795 CAPLUS  
(7) Cebula, T. Journal of Clinical Microbiology 1995, V33, P248 CAPLUS  
(9) Chen, S. Applied Environmental Microbiology 1998, V64, P4210 CAPLUS

ALL CITATIONS AVAILABLE IN THE REFORMAT

L25 ANSWER 14 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1999:227738 CAPLUS  
DOCUMENT NUMBER: 131:40287  
TITLE: Strategies for automated sample preparation, nucleic acid purification, and concentration of low target number nucleic acids in environmental and food processing samples  
AUTHOR(S): Bruckner-Lea, Cynthia J.; Holman, David A.; Schuck,

Beatrice L.; Brockman, Fred J.; Chandler, Darrell P.  
CORPORATE SOURCE: Pacific Northwest National Laboratory, Chemical  
Sensors and Microanalytical Systems, Richland, WA,  
99332, USA  
Proc. SPIE-Int. Soc. Opt. Eng. (1999) 3544(Pathogen  
Detection and Remediation for Safe Eating), 63-71  
CODEN: PSISDG; ISSN: 0277-786X  
SPIE-The International Society for Optical Engineering

SOURCE:

DETECTION AND REMEDIATION FOR SAFE EATING, 63-71  
CODEN: PSISDG; ISSN: 0277-786X  
SPIE-INT. SOC. OPT. ENG. (1999) 3544(PATHOGEN  
DETECTION AND REMEDIATION FOR SAFE EATING)

PUBLISHER:

Journal

DOCUMENT TYPE:

English

Journal

LANGUAGE:

English

AB The purpose of this work is to develop a rapid, automated system for nucleic acid purifi. and concn. from environmental and food processing samples. Our current approach involves off-line filtration and cell lysis (ballistic disintegration) functions in appropriate buffers followed by automated nucleic acid capture and purifi. on a microcolumn. Phys. cell lysis and enzymatic digestion of nucleic acid followed by automated nucleic acid capture and purifi. on a microcolumn eliminate the need for toxic org. solvents, enzyme digestions or other time-consuming sample manipulations. Within the affinity microcolumn, we have examd. nucleic acid capture and purifi. efficiency with various microbead matrices (glass, polymer, paramagnetic), surface derivatization (sequence-specific capture oligonucleotides or peptide nucleic acids), and DNA target size and concn. under variable soln. conditions and temps. Results will be presented comparing automated system performance relative to benchtop procedures for both clean (pure DNA from a lab. culture) and environmental (soil ext.) samples, including results which demonstrate 8 min purifi. and elution of low-copy nucleic acid targets from a crude soil ext. in a form suitable for PCR or microarray-based detectors. Future research will involve the development of improved affinity reagents and complete system integration, including upstream cell concn. and cell lysis functions and downstream, gene-based detectors. Results of this research will ultimately lead to improved processes and instrumentation for online, automated monitors for pathogenic microorganisms in food, water, air, and soil samples.

REFERENCE COUNT: 10

REFERENCE(S): (2) Chandler, D.; Appl Environ Microbiol 1998, V64(2), P669 CAPLUS

(3) Chandler, D.; Mol Ecol 1997, V6(5), P475 CAPLUS

(4) Fry, N.; Appl Environ Microbiol 1997, V63(4), P1498 CAPLUS

(5) Holman, D.; Anal Chem 1997, V69, P1763 CAPLUS

(6) Ruzicka, J.; Anal Chem 1997, V69, P5024 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L25 ANSWER 15 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1998:447631 BIOSIS

DOCUMENT NUMBER: PREV199800447631  
TITLE: Identification of the gene encoding the alternative sigma factor sigmaB from *Listeria monocytogenes* and its role in osmotolerance.

AUTHOR(S): Becker, Lynne A.; Cetin, Mehmet Seyket; Huikins, Robert W.; Benson, Andrew K. (1)

CORPORATE SOURCE: (1) Dep. Food Sci. Technol., 358 Food Industry Complex, Univ. Nebraska, Lincoln, NE 68583-0919 USA  
Journal of Bacteriology, (Sept., 1998) Vol. 180, No. 17,  
pp. 4547-4554.  
ISSN: 0021-9193.

SOURCE:

Journal of Bacteriology

DOCUMENT TYPE:

Article

LANGUAGE:

English

AB *Listeria monocytogenes* is well known for its robust physiology, which permits growth at low temperatures under conditions of high osmolarity and low pH. Although studies have provided insight into the mechanisms used by *L. monocytogenes* to allow the physiological consequences of these adverse environments, little is known about how these responses are coordinated. In the studies presented here, we have cloned the sigB gene and several *rsb* genes from *L. monocytogenes*, encoding homologs of the alternative sigma factor sigmaB and the *RsbUVWX* proteins, which govern transcription of a general stress regulon in the related bacterium *Bacillus subtilis*. The *L. monocytogenes* and *B. subtilis* sigB and *rsb* genes are similar in sequence and physical organization; however, we observed that the activity of sigmaB in *L. monocytogenes* was uniquely responsive to osmotic upshifting, temperature downshifting, and the presence of EDTA in the growth medium. The magnitude of the response was greatest after an osmotic upshift, suggesting a role for sigmaB in coordinating osmotic responses in *L. monocytogenes*. A null mutation in the sigB gene led to substantial defects in the ability of *L. monocytogenes* to use betaine and carnitine as osmoprotectants. Subsequent measurements of betaine transport confirmed that the absence of sigmaB reduced the ability of the cells to accumulate betaine. Thus, sigmaB coordinates responses to a variety of physical and chemical signals, and its function facilitates the growth of *L. monocytogenes* under conditions of high osmotic strength.

L25 ANSWER 16 OF 29 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:524875 CAPLUS

TITLE: Microbial monitoring using hybridization assays and artificial RNA labels.

AUTHOR(S): C. Waia, R. P.; Murphy, J. C.; Fox, G. E.; Willson, R.

CORPORATE SOURCE: Dept Chem Eng, U H Houston, TX, 77204, USA  
Book of Abstracts, 216th ACS National Meeting, Boston,  
August 23-27 (1998), BIOT-223. American Chemical  
Society, Washington, D. C.

SOURCE: August 23-27 (1998), BIOT-223. American Chemical Society, Washington, D. C.

Society, Washington, D. C.



CODEN: 66KYA2  
Conference: Meeting Abstract

DOCUMENT TYPE: English  
LANGUAGE: English

AB Measurement of the nos. and distribution of microorganisms is essential to an understanding of bioremediation, food contamination and microbial pathogenesis. Mol. anal. of reagent populations has been revolutionized by rRNA hybridization-based assays, esp. DNA probe arrays ("DNA chips"). The application of these methods to complex environmental samples requires the extn. of nucleic acids in sufficient purity for anal. We have devised a non-perturbing microbial labeling technique employing Stable Artificial RNAs (SARs), engineered rRNA analogs which display unique identifier sequences and are compatible with DNA chip detection. Many applications of these technologies require development of convenient extn. methods suitable for on-site or field analyses. By exploiting the chem. differences between rRNA and contaminating species such as humic acids, DNA and proteins, we are developing methods of isolating highly pure nucleic acid samples for hybridization anal.

L25 ANSWER 17 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1997:579861 CAPLUS

DOCUMENT NUMBER: 127:215947  
TITLE: Detection of nucleic acid sequence differences using the ligase detection reaction with addressable array

INVENTOR(S): Barany, Francis; Barany, George; Hammer, Robert P.; Kemp, Maria; Blok, Herman; Ziv, Morib  
PATENT ASSIGNEE(S): Cornell Research Foundation, Inc., USA; University of Minnesota; Louisiana State University; Barany, Francis; Barany, George; Hammer, Robert P.; Kemp, Maria; Blok, Herman; Ziv, Morib

SOURCE: PCT Int. Appl., 124 pp.  
CODEN: PIXXD2

DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE  
WO 9731256 A2 19970828 WO 1997-US1535 19970205  
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML,

MR, NE, SN, TD, TG  
CA 2244891 AA 19970828 CA 1997-2244891 19970205  
AU 9727997 A1 19970910 AU 1997-27997 19970205  
EP 920440 A2 19990609 EP 1997-922283 19970205  
R: CH, DE, FR, GB, IT, LI, SE US 1996-11359 19960209

PRIORITY APPLN. INFO.: WO 1997-US1535 19970205

AB The present invention describes a method for identifying one or more of a plurality of sequences differing by one or more single base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences. The method includes a ligation phase, a capture phase, and a detection phase. The ligation phase utilizes a ligation detection reaction between one oligonucleotide probe, which has a target sequence-specific portion and an addressable array-specific portion, and a second oligonucleotide probe having a target sequence-specific portion and a detectable label. After the ligation phase, the capture phase is carried out by hybridizing the target oligonucleotide probes to a solid support with an array of immobilized capture oligonucleotides at least some of which are complementary to the addressable array-specific portion. Following completion of the capture phase, a detection phase is carried out to detect the labels of ligated oligonucleotide probes hybridized to the solid support. The ligation phase can be preceded by an amplification process. The present invention also relates to a kit for practicing this method, a method of forming arrays on solid supports, and the supports themselves.

DUPLICATE 2

L25 ANSWER 18 OF 29 MEDLINE

ACCESSION NUMBER: 97192330 MEDLINE  
DOCUMENT NUMBER: 97192330

TITLE: Molecular diagnostics for dairy-borne pathogens.  
AUTHOR: Batt C A  
CORPORATE SOURCE: Department of Food Science, Cornell University, Ithaca, NY 14853 USA.

SOURCE: JOURNAL OF DAIRY SCIENCE, (1997 Jan) 80 (1) 220-9. Ref: 39  
Journal code: HWV, ISSN: 0022-0302.

PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)

LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199706  
ENTRY WEEK: 19970604

AB Advances in diagnostic assays based on nucleic acids will revolutionize the ability of the industry to maintain the safety of dairy foods

Two complementary assay formats are explored, one of which permits the rapid detection of bacterial pathogens and the other the identification of reservoirs of these pathogens. The first format is an assay based on the polymerase chain reaction that employs homogeneous detection (TaqMan polymerase chain reaction detection, Perkin Elmer, Applied Biosystems Division, Foster City, CA) of the target sequence. This assay has been applied to the detection of *Listeria monocytogenes*. A primary problem with current assays that are based on polymerase chain reaction is the complexity of sample handling and the quantification of the initial target number. This fluorogenic assay takes advantage of the endogenous 5',3'-endonuclease activity in Taq DNA polymerase. Approximately 100 samples can be analyzed in 2 to 3 h with a sensitivity of < 50 cells and a dynamic range of > 1000-fold. The TaqMan polymerase chain reaction detection assay is a robust format that is readily applicable to a wide array of other pathogens found in foods and in the environment. The second format is an instrument for automated ribosomal RNA analysis (Riboprinter, DuPont, Wilmington, DE) that can be used to locate the reservoirs harboring the bacterial pathogen. Use of this typing method it has been shown that, although a number of different ribotypes can be isolated from a single environmental sample, only a selected number of these strains apparently have the ability to cause disease. The future of food microbiology lies in the development and integration of molecular methods that can be automated into a testing regimen that extends from the farm to finished products.

L25 ANSWER 19 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 3  
ACCESSION NUMBER: 1996:363525 BIOSIS

DOCUMENT NUMBER: PREV19969085881  
TITLE: A multiplex PCR for rapid identification of Shiga-like toxin-producing *Escherichia coli* O157:H7 isolated from foods.

AUTHOR(S): Deng, Ming Y.; Fratamico, Pina M. (1)  
CORPORATE SOURCE: (1) Microbial Food Safety Res. Unit, U.S. Dep. Agric., Eastern Regional Res. Cent., Agric. Res. Service, 600 East Mermaid Lane, Wyndmoor, PA 19038 USA  
SOURCE: Journal of Food Protection, (1996) Vol. 59, No. 6, pp. 570-576.

ISSN: 0362-028X.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
AB For rapid and specific identification of enterohemorrhagic *Escherichia coli* (EHEC) serotype O157:H7 isolated from food samples, experimental conditions for a multiplex polymerase chain

reaction (PCR) were optimized and a multiple digoxigenin (DIG)labeled oligonucleotide probe hybridization (DLOPH) assay was developed. A suspect colony from MacConkey sorbitol agar containing 5-bromo-4-chloro-3-indoxyl-beta-D-glucuronide (MSABC/G) was used for the multiplex PCR. Three different DNA sequences of *E. coli* O157:H7 were amplified simultaneously in the PCR: a specific fragment of an attaching and effacing gene (eae gene), conserved sequences of Shiga-like toxins (SLT) I and II, and a fragment of the 60-MDa plasmid. The identities of PCR products were confirmed by hybridization using DIG-labeled internal oligonucleotide probes and colorimetric detection with anti-DIG Fab fragments conjugated to alkaline phosphatase. This method yielded positive results with all reference strains of EHEC serogroup O157, including serotypes O157:H7, O157:NM, and O157:H-, and negative results were obtained with all strains of nontoxigenic *E. coli* serogroup O157, other serotypes of *E. coli*, and other bacterial species. The detection limit of the method was 65 colony-forming units (CFU) of *E. coli* O157:H7. All 29 cultures of EHEC O157:H7 isolated from meat samples and identified by biochemical and serological tests were positive in the multiplex PCR. EHEC O157:H7 was identified from all of 70 experimentally inoculated ground beef and milk samples which had initial inocula of 4 to 9 CFU/g (m) and were subjected to a 6-h enrichment culturing. The multiplex PCR procedure could be very useful for routine examinations of food samples for the presence of EHEC O157.

L25 ANSWER 21 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1997:35735 CAPLUS

DOCUMENT NUMBER: 126:115285  
TITLE: Ultrathin oligonucleotide layers for fluorescence based DNA-sensors

AUTHOR(S): Seeger, S.; Furch, M.; Ueberfeld, J.; Hartmann, A.; Bock, D.;  
CORPORATE SOURCE: Physikalisches-Chemisches Inst., Univ. Heidelberg, Heidelberg, 69120, Germany

SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (1996), 2928(Biomedical Systems and Technologies), 220-226  
CODEN: PSISDG; ISSN: 0277-786X  
PUBLISHER: SPIE-The International Society for Optical Engineering

DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB Preliminary investigations into the design of an affinity sensor using evanescent wave technol. conc. upon the means of immobilization of receptor mols. In this work DNA served as the selective recognition element. The mol. principle of a sequence-selective biosensor for DNA is

based on a sandwich-hybridization assay wherein the analyte, a single-stranded (ss)DNA, bound specifically to both an immobilized capture probe and a dye-labeled oligonucleotide in free soln. The efficiency of the capture array depends on the d. of highly organized oligonucleotides on the waveguide surface and correlates therefore directly with the specificity and the sensitivity of the sensor. In the present approach using the Langmuir-Blodgett technique cinnamoylbutyl/ether-cellulose monolayers were transferred onto optical fibers or planar waveguides. These films served as matrices for the immobilization of biotinylated oligonucleotides via streptavidin. For the first time streptavidin was immobilized by that manner. The specificity of the streptavidin layer or the following bounded nucleic acid moieties, were controlled by an ELISA. Finally, this application has also shown to be suitable for the detection of *Salmonella*, which is an important pathogen associated with acute gastroenteritis and food borne diseases.

L25 ANSWER 22 OF 29 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1995:781986 CAPLUS  
DOCUMENT NUMBER: 123:220262  
TITLE: A method for identifying microorganisms based on nucleic acid amplification and gel electrophoresis

INVENTOR(S): Fluit, Adriana Camille; Widdiglatmodio, Myra Noorely  
PATENT ASSIGNEE(S): U-Gen Research B.V., Neth.  
SOURCE: PCT Int. Appl., 34 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent

LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9513396	A2	19950518	WO 1994-NL283	19941111
WO 9513396	A3	19950608		
W: CA, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
NL 9301957	A	19950601	NL 1993-1957	19931111
NL 1993-1957				

PRIORITY APPL. INFO.:  
AB A method is provided for the identification of a microorganism, in particular a bacterium, present in a sample. Nucleic acid (DNA or RNA) of the microorganism present in the sample is subjected to PCR or a different nucleic acid amplification method, utilizing one or more sets of universal primers based on a gene of the microorganism to be identified which comprises both conserved and

variable regions (in particular the 16 S rRNA gene), the primers being chosen in conserved areas which enclose a variable region. The product of the amplification is brought into single-stranded form, if necessary, and subjected to electrophoresis by which single-stranded nucleic acids of equal lengths can be separated from each other on the basis of differences in nucleotide sequence. The electrophoresed nucleic acids of known position compared with those of a set of reference nucleic acids of known position. Set of suitable aids for practicing the method are provided. Thus, when a PCR primer pair based on regions 103-119 and 341-347 of the 16 S rRNA gene is applied to 114 bacterial strains selected from 40 species and 15 genera, the 35 different single-stranded DNA band patterns that result are species-specific. Multiplex PCR with a second primer set allowed additional discrimination. SSDM (sequence-dependent differences in mobility)-PCR using fluorescein isothiocyanate-labeled primers followed by anal. on an automatic sequencer also yielded species-dependent patterns.

L25 ANSWER 23 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1994:332233 BIOSIS  
DOCUMENT NUMBER: PREV199497345233  
TITLE: Multiplex PCR DNA amplification and gene probe methods for species-specific simultaneous detection of enteropathogenic/toxicogenic, enterohemorrhagic, and enteroinvasive *Escherichia coli* in artificially contaminated ground beef.

AUTHOR(S): Lett, P.; Jones, D. D.; Bei, A. K.  
CORPORATE SOURCE: Dep. Biol., Univ. Ala. at Birmingham, AL 35294-1170 USA  
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (1994) Vol. 94, No. 0, pp. 386.  
Meeting Info.: 94th General Meeting of the American Society for Microbiology Las Vegas, Nevada, USA May 23-27, 1994  
ISSN: 1060-2011.

DOCUMENT TYPE: Conference  
LANGUAGE: English

L25 ANSWER 24 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1993:377181 BIOSIS  
DOCUMENT NUMBER: PREV199345048606  
TITLE: Detection of *Salmonella* spp., *Vibrio cholerae*, and *Vibrio vulnificus* from artificially contaminated shellfish by multiplex polymerase chain reactions (PCR) and gene probes.

AUTHOR(S): Bei, A. K.; Jones, D. D.  
CORPORATE SOURCE: Univ. Alabama Birmingham, Birmingham, AL 35294-1170 USA  
SOURCE: Abstracts of the General Meeting of the American Society

for Microbiology, (1993) Vol. 93, No. 0, pp. 384.  
Meeting info.: 93rd General Meeting of the American Society  
for Microbiology Atlanta, Georgia, USA May 16-20, 1993  
ISSN: 1060-2011.

DOCUMENT TYPE: Article  
LANGUAGE: English

L25 ANSWER 25 OF 29 MEDLINE MEDLINE  
ACCESSION NUMBER: 93119133  
DOCUMENT NUMBER: 93119133  
TITLE: Rapid and sensitive method for detection of Shiga-like  
toxin-producing *Escherichia coli* in ground beef using the  
polymerase chain reaction.

AUTHOR: Gannon V P, King R K, Kim J Y, Thomas E J  
CORPORATE SOURCE: Animal Diseases Research Institute, Agriculture Canada,  
Lethbridge, Alberta.  
APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1992 Dec) 58

SOURCE: (12)  
3809-15.  
Journal code: 6K6, ISSN: 0099-2240.

PUB. COUNTRY: United States  
Journal: Article: (JOURNAL ARTICLE)

LANGUAGE: English  
Priority Journals

FILE SEGMENT: 199304

ENTRY MONTH: AB A rapid and sensitive method for detection of Shiga-like toxin  
(SLT)-producing *Escherichia coli* (SLT-EC) with the polymerase chain  
reaction (PCR) is described. Two pairs of oligonucleotide primers  
homologous to SLT I and SLT II genes, respectively, were used in  
multiplex PCR assays. The first pair generated a ca. 600-bp PCR  
product with DNA from all SLT I-producing *E. coli* tested but not from *E. coli*  
strains that produce SLT II or variants of SLT II. The second pair  
generated a ca. 800-bp PCR product with DNA from *E. coli* strains that  
produce SLT II or variants of SLT II but not from SLT I-producing *E. coli*.  
When used in combination, the SLT I and SLT II oligonucleotide primers  
amplified DNA from all of the SLT-EC tested. No PCR products were obtained  
with SLT primers with DNA from 28 *E. coli* strains that do not produce SLT  
or 44 strains of 28 other bacterial species. When ground beef  
samples were inoculated with SLT-EC strains 319 (O157:H7, SLT I and SLT II),  
H30 (O26:H11, SLT I), and B2F1/3 (O91:H21, SLT II variants VT2ha and VT2hb)  
and cultured in modified trypticase soy broth for 6 h at 42 degrees C, an  
initial sample inoculum of as few as 1 CFU of these SLT-EC strains per g  
could be detected in PCR assays with DNA extracted from the broth  
cultures.

STN more searching 09/6339390 Dec. 11, 2000  
databases searched, search terms, selected abstracts

=> d his  
(FILE HOME: ENTERED AT 15:35:26 ON 11 DEC 2000)  
(FILE MEDLINE, BIOSIS, AGRICOLA, CAPLUS: ENTERED AT 15:35:34 ON 11

DEC

2000  
L1 813524 S FOOD OR FOODBORNE  
L2 115854 S ARRAY? OR MICROARRAY?  
L3 1873 S L1 AND L2  
L4 1619592 S SPECIES  
L5 245 S L1 AND L2 AND L3 AND L4  
L6 237507 S AUTOMAT?  
L7 77911 S DATABASE?  
L8 2 S L5 AND L6  
L9 1844375 S OLIGONUCLEOTIDE? OR DNA OR NUCLEIC(W)ACID?  
L10 117206 S RIBOSOMAL  
L11 13283 S L2 AND (L9 OR L10)  
L12 70 S L11 AND L1  
L13 52 DUP REM L12 (18 DUPLICATES REMOVED)  
L14 37 S L13 AND PY<2000

=> d ibib ab 114 1-

YOU HAVE REQUESTED DATA FROM 37 ANSWERS - CONTINUE? Y/(N)/Y

L14 ANSWER 1 OF 37 MEDLINE  
ACCESSION NUMBER: 2000126777 MEDLINE  
DOCUMENT NUMBER: 20126777  
TITLE: Future trends in diagnosis using laboratory-on-a-chip technologies.  
AUTHOR: Talary M S; Burt J P; Pethig R  
CORPORATE SOURCE: Institute of Molecular and Biomolecular Electronics, University of Wales, Bangor, U.K.  
SOURCE: PARASITOLOGY, (1998) 117 Suppl S191-203. Ref: 11  
Journal code: ORO. ISSN: 0031-1820.  
PUB. COUNTRY: ENGLAND: United Kingdom  
Journal: Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200005

ENTRY WEEK: 20000501

AB There has been an enormous growth in the development of biotechnological applications, where advances in the techniques of microelectronic fabrication and the technologies of miniaturization and integration of semiconductor industries are being applied to the production of Laboratory-on-a-Chip devices. The aim of this development is to create devices that will perform the same processes that are currently carried out in the laboratory in reduced timescales, at a lower cost, requiring less reagents, and with a greater resolution of detection and specificity. The expectations of this Laboratory-on-a-Chip revolution is that this technology will facilitate rapid advances in gene discovery, genetic mapping and gene expression with broader applications ranging from infectious diseases and cancer diagnostics to food quality and environmental testing. A review of the current state of development in this field reveals the scale of the ongoing revolution and serves to highlight the advances that can be perceived in the development of Laboratory-on-a-Chip technologies. Since miniaturization can be applied to such a wide range of laboratory processes, some of the sub-units that can be used as building blocks in these devices are described, with a brief description of some of the fabrication processes that can be used to create them.

L14 ANSWER 2 OF 37 MEDLINE  
ACCESSION NUMBER: 2000000190 MEDLINE  
DOCUMENT NUMBER: 20000190  
TITLE: DNA-microarrays and food biotechnology.  
AUTHOR: Kuipers O P; de Jong A; Holsappel S; Bron S; Kok J; Hamoen L W

CORPORATE SOURCE: Department of Genetics, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Haren, The Netherlands.. o.p.kuipers@biol.rug.nl  
ANTONIE VAN LEEUWENHOEK, (1999 Jul-Nov) 76 (1-4)

SOURCE: 353-5.  
Journal code: GJE. ISSN: 0003-6072.

PUB. COUNTRY: Netherlands  
Journal: Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200001  
ENTRY WEEK: 20000104

L14 ANSWER 3 OF 37 MEDLINE  
ACCESSION NUMBER: 1999439582 MEDLINE  
DOCUMENT NUMBER: 99439582

TITLE: Genomics for food biotechnology: prospects of the use of high-throughput technologies for the improvement of food microorganisms.

AUTHOR: Kuipers O P  
CORPORATE SOURCE: Department of Genetics Groningen Biomolecular Sciences and

Biotechnology Institute University of Groningen PO Box 14,  
9750 AA, Haren, The Netherlands. o.p.kuipers@biol.rug.nl  
CURRENT OPINION IN BIOTECHNOLOGY, (1999 Oct) 10

SOURCE: (5) 511-6. Ref: 45  
Journal code: A92. ISSN: 0958-1669.

PUB. COUNTRY: ENGLAND. United Kingdom  
Journal: Article. (JOURNAL ARTICLE)  
General Review. (REVIEW)  
(REVIEW, TUTORIAL)

LANGUAGE: English  
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200002

ENTRY WEEK: 20000204

AB: Functional genomics is currently the most effective approach for increasing the knowledge at the molecular level of metabolic and adaptive processes in whole cells. High-throughput technologies, such as DNA microarrays, and improved two-dimensional electrophoresis methods combined with tandem mass-spectroscopy, supported by bioinformatics, are useful tools for food biotechnology, which depends on detailed knowledge of the properties of food microbes (and pathogens) in their industrial, food and consumer environments. Genomics of food microbes, based on rapidly emerging genome sequence information, generates valuable knowledge that can be used for metabolic engineering, improving cell factories and development of novel preservation methods. Furthermore, pre- and probiotic studies, characterization of stress responses, studies of microbial ecology and, last but not least, development of novel risk assessment procedures will be facilitated.

L14 ANSWER 4 OF 37 MEDLINE  
ACCESSION NUMBER: 1999147213 MEDLINE

DOCUMENT NUMBER: 99147213

TITLE: Chemoselective biosensors.

AUTHOR: Lowe C R  
CORPORATE SOURCE: Institute of Biotechnology, University of Cambridge, Tennis Court Road, Cambridge CB2 1QT, UK. crt1@biotech.cam.ac.uk  
CURRENT OPINION IN CHEMICAL BIOLOGY, (1999 Feb) 3

SOURCE: (1) 106-11. Ref: 60  
Journal code: CAU. ISSN: 1367-5931.

PUB. COUNTRY: ENGLAND. United Kingdom

Journal: Article. (JOURNAL ARTICLE)  
General Review. (REVIEW)  
(REVIEW, TUTORIAL)

LANGUAGE: English  
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199906

ENTRY WEEK: 19990604

AB: New opportunities for biosensors are now appearing in clinical and genetic diagnostics, genomics, environmental protection, food processing and safety, drug discovery and bioprocess monitoring. Concerns about the cost, stability and selectivity of previous sensor technologies are being addressed by developing new recognition systems and their integration into transducers, micro- and nanofabricated devices, array technologies and novel magnetic, acoustic and optical transduction systems.

L14 ANSWER 6 OF 37 MEDLINE  
ACCESSION NUMBER: 97192330 MEDLINE

DOCUMENT NUMBER: 97192330

TITLE: Molecular diagnostics for dairy-borne pathogens.

AUTHOR: Batt C A

CORPORATE SOURCE: Department of Food Science, Cornell University, Ithaca, NY 14853, USA.  
JOURNAL OF DAIRY SCIENCE, (1997 Jan) 80 (1)

SOURCE: 220-9. Ref: 39  
Journal code: HWV. ISSN: 0022-0302.

PUB. COUNTRY: United States  
Journal: Article. (JOURNAL ARTICLE)  
General Review. (REVIEW)  
(REVIEW, TUTORIAL)

LANGUAGE: English  
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199706

ENTRY WEEK: 19970604

AB: Advances in diagnostic assays based on nucleic acids will revolutionize the ability of the industry to maintain the safety of dairy foods. Two complementary assay formats are explored, one of which permits the rapid detection of bacterial pathogens and the other the identification of reservoirs of these pathogens. The first format is an assay based on the polymerase chain reaction that employs homogeneous detection (TaqMan polymerase chain reaction detection, Perkin Elmer, Applied Biosystems Division, Foster City, CA) of the target sequence. This assay has been applied to the detection of *Listeria monocytogenes*. A primary problem with current assays that are based on polymerase chain reaction is the complexity of sample handling and the quantification of

the initial target number. This fluorogenic assay takes advantage of the endogenous 5',3'-endonuclease activity in Taq DNA polymerase. Approximately 100 samples can be analyzed in 2 to 3 h with a sensitivity of < 50 cells and a dynamic range of > 1000-fold. The TaqMan polymerase chain reaction detection assay is a robust format that is readily applicable to a wide array of other pathogens found in foods and in the environment. The second format is an instrument for automated ribosomal RNA analysis (RiboPrinter, DuPont, Wilmington, DE) that can be used to locate the reservoirs harboring the bacterial pathogen. Use of this typing method it has been shown that, although a number of different ribotypes can be isolated from a single environmental sample, only a selected number of these strains apparently have the ability to cause disease. The future of food microbiology lies in the development and integration of molecular methods that can be automated into a testing regimen that extends from the farm to finished products.

L14 ANSWER 18 OF 37 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1990:131035 BIOSIS  
DOCUMENT NUMBER: BA89:69846

TITLE: SCREENING DNA PROBES USING THE HYDROPHOBIC GRID-MEMBRANE FILTER.

AUTHOR(S): PETERKIN P. I.; IDZIAK E. S.; SHARPE A. N.  
CORPORATE SOURCE: BUREAU MICROBIAL HAZARDS, HEALTH PROTECTION BRANCH HEALTH AND WELFARE CAN., TUNNEY'S PASTURE, OTTAWA, CAN. K1A 0L2.

FOOD MICROBIOL. (LOND), (1989) 6 (4), 281-284.

SOURCE: CODEN: FOMIE5, ISSN: 0740-0020.

FILE SEGMENT: BA: OLD  
LANGUAGE: English

AB Seven clones showing beta-hemolysis, from a *Listeria monocytogenes* genomic library, were assessed by a hydrophobic grid-membrane filter (HGMF) screening technique for their specificity as DNA probes. Plasmid DNA from each of the clones was screened by colony hybridization against replicates of a library of 100 organisms, consisting of 70 *L. monocytogenes* strains, ten other *Listeria* spp., and 20 organisms of other genera, arrayed on an HGMF. Clones showing potential for use in analytical food microbiology were identified by this means.

L14 ANSWER 21 OF 37 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1999:227738 CAPLUS

DOCUMENT NUMBER: 131-40287  
TITLE: Strategies for automated sample preparation.

nucleic acid purification, and concentration of low target number nucleic acids in environmental and food processing samples

AUTHOR(S):

Bruckner-Lea, Cynthia J.; Holman, David A.; Schuck, Beatrice L.; Brockman, Fred J.; Chandler, Darrell P.

CORPORATE SOURCE: Pacific Northwest National Laboratory, Chemical Sensors and Microanalytical Systems, Richland, WA, 99352, USA

SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (1999), 3544/Pathogen Detection and Remediation for Safe Eating), 63-71

CODEN: PSISDG, ISSN: 0277-786X  
SPIE-The International Society for Optical Engineering

PUBLISHER: DOCUMENT TYPE: English Journal

LANGUAGE: AB The purpose of this work is to develop a rapid, automated system for nucleic acid purifi. and concn. from environmental and food processing samples. Our current approach involves off-line filtration and cell lysis (ballistic disintegration) functions in appropriate buffers followed by automated nucleic acid capture and purifi. on renewable affinity matrix microcolumns. Phys. cell lysis and renewable affinity microcolumns eliminate the need for toxic org. solvents, enzyme digestions or other time-consuming sample manipulations. Within the renewable affinity microcolumn, we have exand nucleic acid capture and purifi. efficiency with various microbead matrices (glass, polymer, paramagnetic), surface derivatization (sequence-specific capture oligonucleotides or peptide nucleic acids), and DNA target size and concn. Results will be presented under variable soln. conditions and temps. Results will be presented comparing automated system performance relative to benchtop procedures for both clean (pure DNA from a lab. culture) and environmental (soil ext.) samples, including results which demonstrate 8 min purifi. and elution of low-copy nucleic acid targets from a crude soil ext. in a form suitable for PCR or microarray-based detectors. Future research will involve the development of improved affinity reagents and complete system integration, including upstream cell concn. and cell lysis functions and downstream, gene-based detectors. Results of this research will ultimately lead to improved processes and instrumentation for online, automated monitors for pathogenic microorganisms in food, water, air, and soil samples.

REFERENCE COUNT: 10  
REFERENCE(S): (2) Chandler, D; Appl Environ Microbiol 1998, V64(2),

P669 CAPLUS

(3) Chandler, D; Mol Ecol 1997, V6(5), P475 CAPLUS

(4) Fry, N; Appl Environ Microbiol 1997, V63(4), P1498

CAPLUS  
(5) Holman, D.; Anal Chem 1997, V69, P1763 CAPLUS  
(6) Ruzicka, J.; Anal Chem 1997, V69, P5024 CAPLUS  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 24 OF 37 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:524875 CAPLUS

TITLE: Microbial monitoring using hybridization assays and artificial RNA labels.

AUTHOR(S): C. Walla, R. P. Murphy, J. C. Fox, G. E. Willson, R.

CORPORATE SOURCE: Dept Chem Eng, U H, Houston, TX, 77204, USA

SOURCE: Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (1998), BIOT-223, American Chemical Society, Washington, D. C.

CODEN: 66KYAZ

CONFERENCE: Meeting Abstract

DOCUMENT TYPE: English

LANGUAGE: English

AB Measurement of the nos. and distribution of microorganisms is essential to an understanding of bioremediation, food contamination and microbial pathogenesis. Mol. anal. of recalcitrant populations has been revolutionized by rRNA hybridization-based assays, esp. DNA probe arrays ("DNA chips"). The application of these methods to complex environmental samples requires the exn. of nucleic acids in sufficient purity for anal. We have devised a non-perturbing microbial labeling technique employing Stable Artificial RNAs (SAR's), engineered RNA analogs which display unique identifier sequences and are compatible with DNA chip detection. Many applications of these technologies require development of convenient extrn. methods suitable for on-site or field analyses. By exploiting the chem. differences between rRNA and contaminating species such as humic acids, DNA and proteins, we are developing methods of isolating highly pure nucleic acid samples for hybridization anal.

L14 ANSWER 25 OF 37 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:42541 CAPLUS

DOCUMENT NUMBER: 128:72663

TITLE: Broad specificity affinity arrays: a qualitative approach to complex sample discrimination

INVENTOR(S): Fredrik Mecklenburg, Michael; Danielsson, Bengt; Winquist, Fredrik

PATENT ASSIGNEE(S): Interactiva Biotechnologie G.m.b.H., Germany; Mecklenburg, Michael; Danielsson, Bengt; Winquist, Fredrik

SOURCE: PCT Int. Appl., 29 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 97/49989	A2	1997/12/31	WO 1997-EP3317	1997/06/24 <--

W: AU, CA, JP, US

RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

SE 9602545 A 1997/12/26 SE 1996-2545 1996/06/25 <--

CA 2258941 A 1997/12/31 CA 1997-2258941 1997/06/24 <--

AU 9734363 A1 1998/01/14 AU 1997-34363 1997/06/24

EP 1021713 A2 2000/07/26 EP 1997-930394 1997/06/24

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AB Described is a method for discriminating complex biol. samples using an array of discrete biol. sensing elements immobilized onto a solid support in which constituents bound to the sensor array are directly dectd. by measuring the mass increase on the surface; data anal. of said method is performed using neural network or statistical based pattern recognition techniques. In a preferred embodiment the liq. sample is tested for the presence of sol. constituent(s) by contacting said sample with said sensor array under specific conditions, removing unbound sample constituent(s), deig. the mass increase on the surface and comparing said mass increase data with a ref. std. using pattern recognition software.

L14 ANSWER 26 OF 37 CAPLUS COPYRIGHT 2000 ACS

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TITLE: Detection of nucleic acid sequence differences using the ligase detection reaction with addressable array

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CA 2244891 AA 19970828 CA 1997-2244891 19970205 <-  
AU 9727997 A1 19970910 AU 1997-27997 19970205 <-  
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AB The present invention describes a method for identifying one or more of a plurality of sequences differing by one or more single base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences. The method includes a ligation phase, a capture phase, and a detection phase. The ligation phase utilizes a ligation detection reaction between one oligonucleotide probe, which has a target sequence-specific portion and an addressable array -specific portion, and a second oligonucleotide probe, having a target sequence-specific portion and a detectable label. After the ligation phase, the capture phase is carried out by hybridizing the ligated oligonucleotide probes to a solid support with an array of immobilized capture oligonucleotides at least some of which are complementary to the addressable array -specific portion. Following completion of the capture phase, a detection phase is carried out to detect the labels of ligated oligonucleotide probes hybridized to the solid support. The present invention also relates to a kit for practicing this method, a method of forming arrays on solid supports, and the supports themselves.

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TITLE: Ultrathin oligonucleotide layers for fluorescence based DNA-sensors  
Furch, M.; Ueberfeld, J.; Hartmann, A.; Bock, D.;  
AUTHOR(S): Seeger, S.  
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Heidelberg, 69120, Germany  
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AB Preliminary investigations into the design of an affinity sensor using evanescent wave technol. conc. upon the means of immobilization of the receptor moles. In this work DNA served as the sequence-selective biosensor for DNA is based on a sandwich-hybridization assay wherein the recognition element. The mol. principle of a sequence-selective biosensor is a single-stranded (ss)DNA, bound specifically to both an immobilized capture probe and a dye-labeled oligonucleotide in free soln. The efficiency of the capture array depends on the d. of highly organized oligonucleotides on the waveguide surface and correlates therefore directly with the specificity and the sensitivity of the sensor. In the present approach using the Langmuir-Blodgett technique cinnamoylbutyler-cellulose monolayers were transferred onto optical fibers or planar waveguides. These films served as matrices for the immobilization of biotinylated oligonucleotides via streptavidin. For the first time streptavidin was immobilized by that manner. The specificity of the oligonucleotide probes hybridized to the solid support. The present invention also relates to a kit for practicing this method, a method of forming arrays on solid supports, and the supports themselves.